Modelling wheat behaviour under different population densities using the stochastic GreenLab model

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Introduction

Plant architecture is determined by both the genetic basis of the plant (e.g. Wang and Li, 2006) and the effects of environmental factors (e.g. Evers et al., 2006). It can be described in terms of the dynamics of buds, with the fate of buds depending on their relative positions in space and time (Buck-Sorlin and Bell, 2000). The variation in architecture is obvious in wheat plants (*Triticum aestivum* L.), especially regarding the degree of tillering and consequently yield per plant (Darwinkel, 1978). Deterministic functional-structural plant models (FSPMs) are limited in the simulation of plasticity in development in terms of bud behaviour.

In the current study, the difference and statistical similarity of individual wheat architectures are taken into account in the context of the function-structural model GreenLab. The aim of this paper is to simulate the stochastic development and mean production of wheat plants grown with different population densities, based on calibration of a stochastic GreenLab model. The results are validated with independent data.

Experiment setup and data collection

Two successive experiments have been conducted in the same growth chamber with identical climate conditions in Wageningen, the Netherlands. Spring wheat plants (cv. Minaret) were grown in containers. Seeds were sown at population densities of 100 plants m^{-2} in experiment 1, and 100, 262 and 508 plants m^{-2} in experiment 2. In both experiments, six plants per population density per sampling occasion (four sampling occasions in total) were dissected destructively. Measured data included the dimensions and/or weights of leaf blades, sheaths, internodes, ears and roots. The harvest criteria of the two experiments were similar. Leaf state (appearance, growing, full-grown, dead) was monitored two or three times per week for main stem as well as primary tillers (Exp. 1) or of all orders (Exp. 2), on six plants per population density.

Stochastic GreenLab model

GreenLab (Yan et al. 2004) is a functional-structural model that has been calibrated for different crops. The stochastic GreenLab model (GL2) extends the potential of model applications by introducing bud probabilities (see below) (de Reffye et al. 1988) into its architectural part. Despite its complexity, the analytical output of this stochastic functional-structural model (mean and variance of organ number, as well as mean product of plant) has been computed (Kang et al., 2007a).

Compared to the deterministic GreenLab model for wheat (Kang et al., 2007b), in GL2, the *bud breakout probability* (P_b) describes the chance that a bud develops into a tiller. The *tiller survival probability* (P_f) describes the chance that a tiller survives and ultimately bears an ear. The probabilities can be different for main stem and tillers of different order. The third probability is *phytomer growth probability* (P_g). It is introduced as tillers often contain less and variable phytomers compared to the potential pattern (Bos and Neuteboom, 1998) which is the upper boundary of the topological structure.

Model calibration

The parameters to be calibrated consist of two parts: (I) the bud probabilities and (II) the parameters describing sink and source functions. For (I), the fitting targets are (a) the mean and variance of the total number of phytomers from the emergence to the appearance of the flag leaf; these data were obtained from the record on leaf state on six plants; (b) the mean and variance of number of ears at grain-filling stage. For (II), the fitting targets are the mean weight of organs at each phytomer rank for main stem and tillers, obtained from the destructive measurement at the four sampling stages.

A non-linear least square method is used to minimize the root mean square error between the fitting targets and the model output, the latter being functions of model parameters. To compute the numerical output for a stochastic model with Monte-Carlo simulation is time-consuming. In contrast, the analytical results of the stochastic GreenLab model (Kang et al., 2007a) provide a fast and precise way to do the computations with recurrent equations.

Preliminary results

The analytical mean and variance of number of organs computed with methods described in Kang et al. (2007a), are close to the measured data from Exp. 1 (densities 100 plants m^{-2}), see Figs. 1 and 2. The fitting process resulted in a set of bud probabilities (Table 1) for each population density. Using mean organ number, the model computed the mean value of organ weight along the phytomer position at each plant age (in growth cycles). This output fitted well to the measured data (figures and parameters shown in later communications). The stochastic GreenLab model is a promising tool to simulate wheat samples of which the architecture and product vary with population density.

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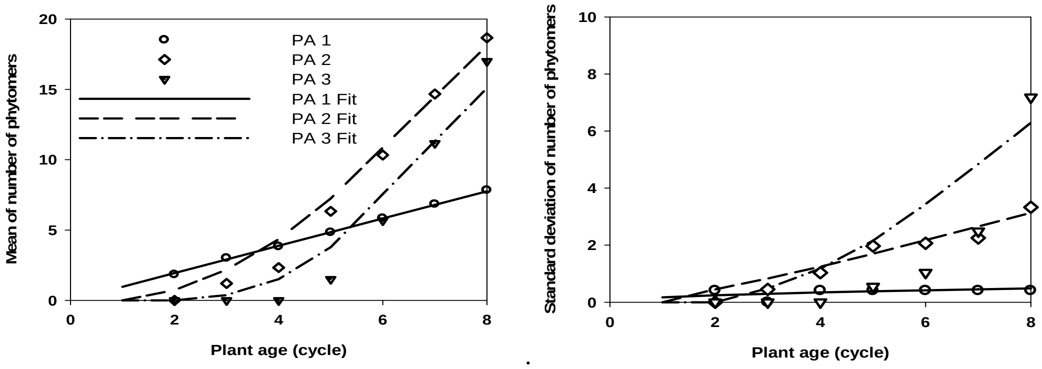
Table 1. Estimated bud probabilities for each population density in Exp. 2, of the main stem (PA 1), primary tillers (PA 2) and secondary tillers (PA 3). The tiller bud break probability for PA 1 is the seed emergence probability.

Density (plants m^{-2})	Bud break probability P_b			Phytomer growth probability P_a			Tiller survival probability P_f		
	PA 1	PA 2	PA 3	PA 1	PA 2	PA 3	PA 1	PA 2	PA 3
100	0.85	0.95	0.97	0.78	0.91	0.91	0.92	0.79	0.47
262	0.76	0.89	1.00	0.69	0.61	0.61	1.00	0.52	0.08
508	0.79	0.45	0.97	0.80	0.42	0.42	1.00	0.34	0.00



(a) (b)

Fig.1. The mean (a) and standard deviation (b) of the number of phytomers in main stem (PA 1), primary tillers (PA 2), secondary tillers (PA 3) of a wheat plant at each plant age (in growth cycles), at a population density of 100 plants m^{-2}, from observation (symbols) and model output (lines).

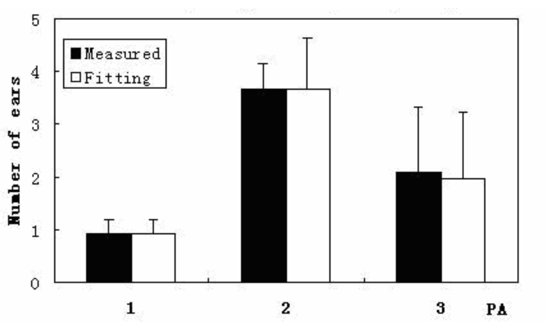


Fig.2. The mean and standard deviation of the number of final ears in main stem (PA 1), primary tillers (PA 2), secondary tillers (PA 3).